

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hawkins, Phillip R.
Murry, Lynn E.
- (ii) TITLE OF THE INVENTION: HUMAN PHOSPHOLIPASE INHIBITOR
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: U.S.
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Luther, Barbara J.
(B) REGISTRATION NUMBER: 33,954
(C) REFERENCE/DOCKET NUMBER: PF-0059-1 US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 839 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1LPB02
(B) CLONE: CONSENSUS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

NCAATGGGCC GGCCGTGGGA AGGGTGAATG TGGGTCCAGA CCCGCCCCCTC CTCAGCTTCC

09875520-060604

TATAAAAGCT	GGGGACCAGG	TACTGCTGAT	ACACACACCA	TGAGGCTCTC	CAGGAGACCA	120
GAGACCTTTC	TGCTGGCCTT	TGTGTTGCTC	TGCACCCTCC	TGGGTCTTGG	GTGCCCCACTA	180
CACTGCGAAA	TATGTACGGC	GGCGGGGAGC	AGGTGCCATG	GCCAAATGAA	GACCTGCAGC	240
AGTGACAAGG	ACACATGTGT	GCTCCTGGTC	GGGAAGGCTA	CTTCAAAGGG	CAAGGAGTTG	300
GTGCACACCT	ACAAGGGCTG	CATCAGGTCC	CAGGACTGCT	ACTCCGGCGT	TATATCCACC	360
ACCATGGGCC	CCAAGGACCA	CATGGTAACC	AGCTCCTTCT	GCTGCCAGAG	CGACGGCTGC	420
AACAGTGCCT	TTTTGTCTGT	TCCCTTGACC	AATCTTACTG	AGAATGGCCT	GATGTGCCCC	480
GCCTGCACTG	CGAGCTTCAG	GGACAAATGC	ATGGGGCCCA	TGACCCACTG	TACTGGAAAG	540
GAAAACCACT	GCGTCTCCTT	ATCTGGACAC	GTGCAGGCTG	GTATTTTCAA	ACCCAGATTT	600
GCTATGCGGG	GCTGTGCTAC	AGAGAGTATG	TGCTTTACCA	AGCCTGGTGC	TGAAGTACCC	660
ACAGGCACCA	ATGTCCTCTT	CCTCCATCAT	ATAGAGTGCA	CTCACTCCCC	CTGAAAAGCT	720
ATCTGAACAG	AGGAAGATAA	TGTAGTGTGA	AGTCCCCATT	TGTCCTCAGC	CTGTAACCTC	780
CCCGTGTGCC	TATAAAGAAG	TTAATAGAGC	AAAAAAAAAA	AAAAAAAAAA	AAACTCGAG	839

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB02
- (B) CLONE: CONSENSUS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Leu	Ser	Arg	Arg	Pro	Glu	Thr	Phe	Leu	Leu	Ala	Phe	Val	Leu
1				5					10					15	
Leu	Cys	Thr	Leu	Leu	Gly	Leu	Gly	Cys	Pro	Leu	His	Cys	Glu	Ile	Cys
			20					25					30		
Thr	Ala	Ala	Gly	Ser	Arg	Cys	His	Gly	Gln	Met	Lys	Thr	Cys	Ser	Ser
			35				40					45			
Asp	Lys	Asp	Thr	Cys	Val	Leu	Leu	Val	Gly	Lys	Ala	Thr	Ser	Lys	Gly
	50				55				60						
Lys	Glu	Leu	Val	His	Thr	Tyr	Lys	Gly	Cys	Ile	Arg	Ser	Gln	Asp	Cys
65				70					75					80	
Tyr	Ser	Gly	Val	Ile	Ser	Thr	Thr	Met	Gly	Pro	Lys	Asp	His	Met	Val
			85					90					95		
Thr	Ser	Ser	Phe	Cys	Cys	Gln	Ser	Asp	Gly	Cys	Asn	Ser	Ala	Phe	Leu
			100				105					110			
Ser	Val	Pro	Leu	Thr	Asn	Leu	Thr	Glu	Asn	Gly	Leu	Met	Cys	Pro	Ala
	115				120						125				
Cys	Thr	Ala	Ser	Phe	Arg	Asp	Lys	Cys	Met	Gly	Pro	Met	Thr	His	Cys
	130				135					140					
Thr	Gly	Lys	Glu	Asn	His	Cys	Val	Ser	Leu	Ser	Gly	His	Val	Gln	Ala
145				150					155					160	
Gly	Ile	Phe	Lys	Pro	Arg	Phe	Ala	Met	Arg	Gly	Cys	Ala	Thr	Glu	Ser
			165				170							175	
Met	Cys	Phe	Thr	Lys	Pro	Gly	Ala	Glu	Val	Pro	Thr	Gly	Thr	Asn	Val
			180				185						190		
Leu	Phe	Leu	His	His	Ile	Glu	Cys	Thr	His	Ser	Pro				
	195						200								

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: GI 501050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Lys	Tyr	Leu	His	Thr	Ile	Cys	Leu	Leu	Phe	Ile	Phe	Val	Ala	Arg	1	5	10	15
Gly	Asn	Ser	Arg	Ser	Cys	Asp	Phe	Cys	His	Asn	Ile	Gly	Lys	Asp	Cys	20	25	30	
Asp	Gly	Tyr	Glu	Glu	Glu	Cys	Ser	Ser	Pro	Glu	Asp	Val	Cys	Gly	Lys	35	40	45	
Val	Leu	Leu	Glu	Ile	Ser	Ser	Ala	Ser	Leu	Ser	Val	Arg	Thr	Val	His	50	55	60	
Lys	Asn	Cys	Phe	Ser	Ser	Ser	Ile	Cys	Lys	Leu	Gly	Gln	Phe	Asp	Val	65	70	75	80
Asn	Ile	Gly	His	His	Ser	Tyr	Ile	Arg	Gly	Arg	Ile	Asn	Cys	Cys	Glu	85	90	95	
Lys	Glu	Leu	Cys	Glu	Asp	Gln	Pro	Phe	Pro	Gly	Leu	Pro	Leu	Ser	Lys	100	105	110	
Pro	Asn	Gly	Tyr	Tyr	Cys	Pro	Gly	Ala	Ile	Gly	Leu	Phe	Thr	Lys	Asp	115	120	125	
Ser	Thr	Glu	Tyr	Glu	Ala	Ile	Cys	Lys	Gly	Thr	Glu	Thr	Lys	Cys	Ile	130	135	140	
Asn	Ile	Val	Gly	His	Arg	Tyr	Glu	Gln	Phe	Pro	Gly	Asp	Ile	Ser	Tyr	145	150	155	160
Asn	Leu	Lys	Gly	Cys	Val	Ser	Ser	Cys	Pro	Leu	Leu	Ser	Leu	Ser	Asn	165	170	175	
Ala	Thr	Phe	Glu	Gln	Asn	Arg	Asn	Tyr	Leu	Glu	Lys	Val	Glu	Cys	Lys	180	185	190	
Asp	Ala	Ile	Arg	Leu	Ala	Ser	Leu									195	200		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HMC1N0T01
(B) CLONE: 8941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAGGCCTAG	GGTTAGGCAA	GACCTTGAGG	CAGGGGTTGA	AGCCAGGGAG	TGGTCAGCCA	60
GCACTGTCCC	TGCCTGTCCC	CATCCCACAG	AGGGCAAGGA	GTTGGTGCAC	ACCTACAAGG	120
GCTGCATCAG	GTCCCAGGAC	TGCTACTCCG	GCCTTATATC	NACCACCATG	GGCCCCAAGG	180
ACCACATGGT	AACCAGCTCC	TTCTGNTGCC	AGAGCGACGG	CTGCAACAGT	GCCTTTTGT	240
CTGTTCCCTT	GACCAATCTT	ACTGAGAATG	GCCTGATGTG	CCCNGCTGCA	CTGCGAGTTT	300
NAGGGNCAAA	ATNCATGGGG	GCCCATT				327

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1LPB01
(B) CLONE: 10033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTGCTCTNC	ACCCTCCTGG	GTCTTGGGTG	CCCACTACAC	TGCGAAATAT	GTACGGCGGC	60
GGGGAGCAGG	TGCCATGGCC	AAATGAAGAC	CTGCAGCAGT	GACAAGGACA	CATGTGTGCT	120
CCTGGTCGGG	AAGGCTACTT	CAAAGGGCAA	GGAGTTGGTG	CACACCTACA	AGGGCTGCAT	180
CAGGTCCCAG	GACTGCTACT	CCGGCGTTAT	ATCCACCACC	ATGGGCCCCA	AGGACCACAT	240
GGTAACCAGC	TCCTTCTGCT	GCAGAGCGAC	GGCTGCAACA	GTGCCTTTTT	GTCTGTTCCC	300
TTGACCAATC	TTACTGAGAA	TGGT				324

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1LPB01
(B) CLONE: 10644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACACATGTG	TNCTCCTGGT	CGGGAAGGCT	ACTTCAAAGG	GCAAGGAGTT	GGTGACACACC	60
TACAAGGGCT	GCATCAGGTN	CCAGGACTGC	TACTCCGGNG	TTATATCCAC	CACCATGGGC	120
CCCAAGGACC	ACATGGTAAC	CAGTCTCTTC	TGCTGCCAGA	GCGACGGCTG	CAACAGTGCC	180

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TTTTTGTCTG TTCCCTTGAC CAATNTTACT GAGAATNGNC TGATGTGCCC CGNCTGCACT 240
GNGAGCTTCA GGGACAAATG CT 262

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB01
- (B) CLONE: 10774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACACATGTG	TGCTCCTGGT	CGGGAAGGCT	ACTTCAAAGG	GCAAGGAGTT	GGTGACACACC	60
TACAAGGGCT	GCATCAGGTC	CCAGGACTGC	TACTCCGGNG	TTATATCCAC	CACCATGGGC	120
CCCAAGGACC	ACATGGTAAC	CAGCTCCTTC	TGCTGCCAGA	GCGACGGCTG	CAACAGTGCC	180
TTTTTGTCTG	TTCCCTTANC	CAATCTTACT	GAGAATGGCC	TGATGTGCCC	CGNCTGAACT	240
NCGAGCTTCA	GGGACAAATN	CATGGGNCNA	TGACCCACTG	TACTGGNAAG	NNAAACCACT	300
GNGTGTCCTT						310

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PEB01
- (B) CLONE: 71854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCCGGCGTT	ATATCCACCA	CCATGGGCCC	CAAGGACCAC	ATGGTAACCA	GCTCCTTCTG	60
CTGCCAGAGC	GACGGCTGCA	ACANTGCCTT	TTTNTNTGTT	CCCTTGACCA	ATCTTACTGA	120
GAATGGCCTG	ATGTGCCCCG	CCTGCACTGC	GAGCTTCAGG	GACAAATGCA	TGGGGCCCAT	180
GACCC						185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(ii) MOLECULE TYPE: cDNA

(A) LIBRARY: THP1PEB01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTGGTGCAC	ACCTACAAGG	GCTGCATCAG	GTCCCAGGAC	TTCTACTCCG	GNGTTATATC	60
CACCACCATG	GGCCCCAAGG	ACCACATGGT	AACCAGCTCC	TTNTGCTGCC	AGAGCGACGG	120
CTGCAACATT	GCCTTTTTNT	NTGTNCCCTT	G			151

(2) INFORMATION FOR SEQ ID NO:10:

(A) LENGTH: 144 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) LIBRARY: THP1PEB01

(B) CLONE: 74452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGACTGCT	ACTCCGGNGT	TATATCCACC	ACCATGGGCC	CCAAGGACCA	CATGGTAACC	60
AGCTCCTTCT	GCTGCCAGAG	CNACGGCTGC	AACANTGCCT	TTNTGTCTGT	NCCCTTGACC	120
AATCTNACTG	AGAATNGCCT	GATT				144

(2) INFORMATION FOR SEQ ID NO:11:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) LIBRARY: THP1LPB02

(B) CLONE: 155045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CNTGGCCTTA	GTTTTNCNCT	CACCCTCCNG	GGTCTNNGGT	GCCCACNACA	CTGCGAANTA	60
TGTACGGCGG	CGGGTAGCAG	GTTCCATGNC	CAAATNAAGA	NCTTCANCNG	TGACAAGGAC	120
ACATGTNTGC	TCCTGGTCGG	NAAGNCTACT	TCAAAGGGCA	AGGAGTTGGT	GCAC	174

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB02
- (B) CLONE: 156817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGGCCTTTG	TGTTGCTCTG	CACCTCCTG	GGTCTTGGGT	GCCCACTACA	CTGCGAAATA	60
TGTACGGCGG	CGGGGAGCAG	GTGCCATGGC	CAAATGAAGA	CCTGCAGCAG	TGACAAGGAC	120
ACATGTGTGC	TCCTGGTCGG	GAAGGCTACT	TCAAAGGGCA	AGGAGTTNGT	GCACACCTAC	180
AAGGGCTGCA	TCAT					194

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PGANNO01
- (B) CLONE: 619856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAAGAGAC	CATNCCAGGA	AGTTGTGGGG	TTGGGGAGGC	CTAGGGTTAG	GCAAGACCTT	60
GAGGCAGGGG	TTGAAGCCAG	GGAGTGGTCA	GCCAGCACTG	TCCCTGCCTG	TCCCCATCCC	120
ACAGAGGGCA	AGGAGTTGGT	GCACAACCTAC	AAGGGCTGCA	TCAGGTCCCA	GGACTGCTAC	180
TNCGGNGTTA	TATCCACCAC	CATGGGCCCC	AAGGACCACA	TGGT		224

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSNO02

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(B) CLONE: 683480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTGGTGCAC	ACCTACAAGG	GCTGCATCAG	GTCCCAGGAC	TGCTACTCCG	GCGTTATATN	60
CACCACCATG	GGNCCCAAGG	ACCACATGGT	AACCAGCTCC	TTNTGCTGCC	AGAGCGACGN	120
CTGCAACAGT	GCCTTTTTGT	CTGTTCCCTT	GACCAATCTT	ACTGAGAATG	GCCTGATGTG	180
CCCCGNCTGC	ACTGCGAGCT	TNAGGGACAA	ATGCATGGGG	CCCATGACCC	ACTGTACTGG	240
AGAGGAAAAC	CA					252

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT11
- (B) CLONE: 1291208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

GGGAATCCCA	GTTCTTGCA	CCACTGGGAA	TCAAGAGGCC	CAACTCCGTC	TTGGTCTTNN	60
NNNNNNNNNN	NNNNNNNNCA	TGGGCCGGCC	GTGGGAAGGG	TGAATGTGGG	TCCAGACCCG	120
CCCCTCCTCA	GCTTCCTATA	AAAGCTGGGG	ACCAGGTA	GCTGATACAC	ACACCATGAG	180
GCTCTCCAGG	AGACCAGAGA	CCTTCTGCT	GGCCTTTGTG	TTGCTCTGCA	CCCTCCTGGG	240
TCTTGGGTGC						250